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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/879,827A

DATE: 01/27/1999
TIME: 15:55:05

INPUT SET: S30367.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Jofuku, K. Diane
Okamuro, Jack K.

(ii) TITLE OF INVENTION: Methods for Improving Seeds

(iii) NUMBER OF SEQUENCES: 111

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Townsend and Townsend and Crew LLP
(B) STREET: Two Embarcadero Center, Eighth Floor
(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94111-3834

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/879,827
(B) FILING DATE: 20-JUN-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/700,152
(B) FILING DATE: 20-AUG-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Bastian, Kevin L.
(B) REGISTRATION NUMBER: 34,774
(C) REFERENCE/DOCKET NUMBER: 023070-067210US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (415) 576-0200
(B) TELEFAX: (415) 576-0300

(2) INFORMATION FOR SEQ ID NO:1:

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47 (i) SEQUENCE CHARACTERISTICS:
48 (A) LENGTH: 3 amino acids
49 (B) TYPE: amino acid
50 (C) STRANDEDNESS:
51 (D) TOPOLOGY: linear
52
53 (ii) MOLECULE TYPE: peptide
54
55
56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
57
58 Tyr Arg Gly
59 1
60
61
62 (2) INFORMATION FOR SEQ ID NO:2:
63
64 (i) SEQUENCE CHARACTERISTICS:
65 (A) LENGTH: 4 amino acids
66 (B) TYPE: amino acid
67 (C) STRANDEDNESS:
68 (D) TOPOLOGY: linear
69
70 (ii) MOLECULE TYPE: peptide
71
72
73 (ix) FEATURE:
74 (A) NAME/KEY: Modified-site
75 (B) LOCATION: 3
76 (D) OTHER INFORMATION: /product= "OTHER"
77 /note= "Xaa = Ala or Ser"
78
79 (ix) FEATURE:
80 (A) NAME/KEY: Modified-site
81 (B) LOCATION: 4
82 (D) OTHER INFORMATION: /product= "OTHER"
83 /note= "Xaa = Arg or His"
84
85
86 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
87
88 Trp Glu Xaa Xaa
89 1
90
91
92 (2) INFORMATION FOR SEQ ID NO:3:
93
94 (i) SEQUENCE CHARACTERISTICS:
95 (A) LENGTH: 1680 base pairs
96 (B) TYPE: nucleic acid
97 (C) STRANDEDNESS: single
98 (D) TOPOLOGY: linear
99

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100 (ii) MOLECULE TYPE: cDNA
101
102
103 (ix) FEATURE:
104 (A) NAME/KEY: -
105 (B) LOCATION: 1..1680
106 (D) OTHER INFORMATION: /note= "Arabidopsis APETALA2 (AP2)"
107
108
109 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
110
111 CTCTCTCTCT CTCTTTAGCT CTTTTTTTTT TTTTGTTC ATTAAGTTT TTATTTTATT 60
112
113 TTCTACCAAC CAAAAGCTTT TCTCTTTGGT TTCTCTTATT TAGCTTCTAA CCTTGAGGAG 120
114
115 AATATACCAG AGGATTGAAG TTTGAACCTT CAAAGATCAA AATCAAGAAA CCAAAAAAAAA 180
116
117 AAAAAAAAAA TGTGGGATCT AAACGACGCA CCACACCAAA CACAAAGAGA AGAAGAATCT 240
118
119 GAAGAGTTTT GTTATTCTTC ACCAAGTAAA CGGGTTGGAT CTTTCTCTAA TTCAAGCTCT 300
120
121 TCAGCTGTTG TTATCGAAGA TGGATCCGAT GACGATGAAC TTAACCGGGT CAGACCCAAT 360
122
123 AACCCACTTG TCACCCATCA GTTCTTCCCT GAGATGGATT CTAACGGCGG TGGTGTGCT 420
124
125 TCTGGCTTTC CTCGGGCTCA CTGGTTTGGT GTTAAGTTTT GTCAGTCGGA TCTAGCCACC 480
126
127 GGATCGTCCG CGGGTAAAGC TACCAACGTT GCCGCTGCCG TAGTGGAGCC GGCACAGCCG 540
128
129 TTGAAAAAGA GTCGGCGTGG ACCAAGATCA AGAAGTTCTC AGTATAGAGG TGTTACGTTT 600
130
131 TACCGGCGTA CCGGAAGATG GGAATCTCAT ATTTGGGACT GTGGGAAACA AGTTTACTTA 660
132
133 GGTGGATTG AACTGCTCA TGCAGCAGCT CGAGCATATG ATAGAGCTGC TATTAAATTC 720
134
135 CGTGGAGTAG AAGCGGATAT CAATTTCAAC ATCGACGATT ATGATGATGA CTTGAAACAG 780
136
137 ATGACTAATT TAACCAAGGA AGAGTTCGTA CACGTACTTC GCCGACAAAG CACAGGCTTC 840
138
139 CCTCGAGGAA GTTCGAAGTA TAGAGGTGTC ACTTTGCATA AGTGTGGTCG TTGGGAAGCT 900
140
141 CGTATGGGTC AATTCTTAGG CAAAAAGTAT GTTTATTTGG GTTTGTTCGA CACCGAGGTC 960
142
143 GAAGCTGCTA GAGCTTACGA TAAAGCTGCA ATCAAATGTA ACGGCAAAGA CGCCGTGACC 1020
144
145 AACTTTGATC CGAGTATTTA CGATGAGGAA CTCAATGCCG AGTCATCAGG GAATCCTACT 1080
146
147 ACTCCACAAG ATCACAACCT CGATCTGAGC TTGGGAAATT CGGCTAATTC GAAGCATAAA 1140
148
149 AGTCAAGATA TCGGGCTCAG GATGAACCAA CAACAACAAG ATTCTCTCCA CTCTAATGAA 1200
150
151 GTTCTTGGAT TAGGTCAAAC CGGAATGCTT AACCATACTC CCAATTCAAA CCACCAATTT 1260
152

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153 CCGGGCAGCA GCAACATTGG TAGCGGAGGC GGATTCTCAC TGTTTCCGGC GGCTGAGAAC 1320
154
155 CACCGGTTTG ATGGTCGGGC CTCGACGAAC CAAGTGTTGA CAAATGCTGC AGCATCATCA 1380
156
157 GGATTCTCTC CTCATCATCA CAATCAGATT TTTAATTCTA CTTCTACTCC TCATCAAAAT 1440
158
159 TGGCTGCAGA CAAATGGCTT CCAACCTCCT CTCATGAGAC CTTCTTGAAT CTTTATATT 1500
160
161 TTTAAGGTTT ATTATTATAT AAGAAAAACA AAAATGAACC TTTGAAATCC CCACATGTTC 1560
162
163 TTGGTCATTT CATTAAATCAT CGGCTTATAT TTTGCTTATT TTCCCCTAAA TCCTCTTGTT 1620
164
165 AACTTAGGCG AACAAAAAAA ATTAATGGAA ATCTTTTTTCC CTCCATCGGT TACAAAAATA 1680
166
167

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: /note= "AP2-R1 direct repeat at positions 129 to 195"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 32..49
- (D) OTHER INFORMATION: /note= "putative AP2-R1 amphipathic alpha-helix (SEQ ID NO:6)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

194 Ser Ser Gln Tyr Arg Gly Val Thr Phe Tyr Arg Arg Thr Gly Arg Trp
195 1          5          10          15
196
197 Glu Ser His Ile Trp Asp Cys Gly Lys Gln Val Tyr Leu Gly Gly Phe
198          20          25          30
199
200 Thr Asp Ala His Ala Ala Ala Arg Ala Tyr Asp Arg Ala Ala Ile Lys
201          35          40          45
202
203 Phe Arg Gly Val Glu Ala Asp Ile Asn Phe Asn Ile Asp Asp Tyr Asp
204          50          55          60
205

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206 Asp Asp Leu
207 65
208
209210 (2) INFORMATION FOR SEQ ID NO:5:
211

212 (i) SEQUENCE CHARACTERISTICS:

213 (A) LENGTH: 68 amino acids
214 (B) TYPE: amino acid
215 (C) STRANDEDNESS:
216 (D) TOPOLOGY: linear
217218 (ii) MOLECULE TYPE: peptide
219
220

221 (ix) FEATURE:

222 (A) NAME/KEY: Peptide
223 (B) LOCATION: 1..68
224 (D) OTHER INFORMATION: /note= "AP2-R2 direct repeat at
225 positions 221 to 288"
226

227 (ix) FEATURE:

228 (A) NAME/KEY: Region
229 (B) LOCATION: 33..50
230 (D) OTHER INFORMATION: /note= "putative AP2-R2 amphipathic
231 alpha-helix (SEQ ID NO:7)"
232
233234 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
235236 Ser Ser Lys Tyr Arg Gly Val Thr Leu His Lys Cys Gly Arg Trp Glu
237 1 5 10 15
238
239 Ala Arg Met Gly Gln Phe Leu Gly Lys Lys Tyr Val Tyr Leu Gly Leu
240 20 25 30
241
242 Phe Asp Thr Glu Val Glu Ala Ala Arg Ala Tyr Asp Lys Ala Ala Ile
243 35 40 45
244
245 Lys Cys Asn Gly Lys Asp Ala Val Thr Asn Phe Asp Pro Ser Ile Tyr
246 50 55 60
247
248 Asp Glu Glu Leu
249 65
250
251252 (2) INFORMATION FOR SEQ ID NO:6:
253

254 (i) SEQUENCE CHARACTERISTICS:

255 (A) LENGTH: 18 amino acids
256 (B) TYPE: amino acid
257 (C) STRANDEDNESS:
258 (D) TOPOLOGY: linear

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SEQUENCE VERIFICATION REPORT
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